

RAW SEQUENCE LISTING

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Application Serial Number: 10/785,607B
Source: 1Fw16
Date Processed by STIC: 11/10/05

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IFW 16

RAW SEQUENCE LISTING

DATE: 11/10/2005

PATENT APPLICATION: US/10/785,607B

TIME: 09:04:12

Input Set : A:\39780-1216R1C1D5 SAVED NOV 1 2005.TXT

Output Set: N:\CRF4\11102005\J785607B.raw

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4 <110> APPLICANT: Ashkenazi, Avi J.
5     Fong, Sherman
6     Goddard, Audrey
7     Gurney, Austin L.
8     Napier, Mary A.
9     Tumas, Daniel
10    Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
13     THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED
14     ANTIGENS
16 <130> FILE REFERENCE: 39780-1216R1C1D5
18 <140> CURRENT APPLICATION NUMBER: US 10/785,607B
19 <141> CURRENT FILING DATE: 2004-02-24
21 <150> PRIOR APPLICATION NUMBER: US 09/953,499
22 <151> PRIOR FILING DATE: 2001-09-14
24 <150> PRIOR APPLICATION NUMBER: US 09/254,465
25 <151> PRIOR FILING DATE: 1999-03-05
27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
28 <151> PRIOR FILING DATE: 1998-11-20
30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
31 <151> PRIOR FILING DATE: 1998-09-17
33 <160> NUMBER OF SEQ ID NOS: 30
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 299
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
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46           20           25           30
47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
48           35           40           45
49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50           50           55           60
51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
52 65           70           75           80
53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
54           85           90           95
55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
56           100          105          110
57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

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58          115          120          125
59 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
60      130          135          140
61 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
62 145          150          155          160
63 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
64          165          170          175
65 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
66          180          185          190
67 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
68          195          200          205
69 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
70      210          215          220
71 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
72 225          230          235          240
73 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
74          245          250          255
75 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
76          260          265          270
77 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
78          275          280          285
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91 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
92          20          25          30
93 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
94          35          40          45
95 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
96          50          55          60
97 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
98 65          70          75          80
99 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
100          85          90          95
101 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
102          100          105          110
103 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
104          115          120          125
105 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
106          130          135          140
107 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
108 145          150          155          160
109 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile

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110          165          170          175
111 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
112          180          185          190
113 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
114          195          200          205
115 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
116          210          215          220
117 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
118 225          230          235          240
119 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
120          245          250          255
121 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
122          260          265          270
123 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
124          275          280          285
125 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
126          290          295          300
127 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
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136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Consensus DNA Sequence
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143 ttgtatggtc tctgaggaag gcggcaacag ctatggggag gtcaaggtca agctcatcgt 120
144 gcttgtgcct ccatccaagc ctacagttaa catcccctcc tctgccacca ttgggaaccg 180
145 ggcagtgctg acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
146 agatgggata gtgatgccta cgaatcccaa aagcaccctg gccttcagca actcttccta 300
147 tgtcctgaat ccacaacag gagagctggt ctttgatccc ctgtcagcct ctgatactgg 360
148 agaatacagc tgtgaggcac ggaatgggta          390
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151 <211> LENGTH: 726
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Consensus DNA Sequence
158 <400> SEQUENCE: 4
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160 ctgttgtgct caggtgcgcc tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac 120
161 tgttgtgcct cttcatattg gcgatcctgt tgtgctccct ggcattgggc agtggttacag 180
162 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtcctgt 240
163 gcctactcgg gcttttcttc tccccgtgtg gagtggaagt ttgaccaagg agacaccacc 300
164 agactcgttt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttcttg 360
165 ccaactggta tcaccttcaa gtccgtgaca cggaagaca ctgggacata cacttgatg 420
166 gtctctgagg aaggcgcaa cagctatggg gaggtcaagg tcaagtcct cgtgcttgtg 480

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167 cctccatcca agcctacagt taacatcccc tcctctgccca ccattgggaa cggggcagtg 540
168 ctgacatgct cagaacaaga tggttcccca ctttctgaat acacctggtt caaagatggg 600
169 atagtgatgc ctacgaatcc caaaagcacc cgtgccttca gcaactcttc ctatgtcctg 660
170 aatcccacaa caggagagct ggtctttgat ccctgtcag cctctgatac tggagaatac 720
171 agctgt 726
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 1503
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Consensus DNA Sequence
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184 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
185 ctctgtctcc aagcccacag tgacaactgg cagcgggttat ggcttcacgg tgccccaggg 240
186 aatgaggatt agccttcaat gccagggttc ggggttctcc tcccatcagt tatatttgg 300
187 ataagcaaca gactaataac cagggaaccc atcaaagtag caaccctaag taccttactc 360
188 ttcaagcctg cggatgatagc cgactcaggc tcctatttct gcactgcaa gggccaggtt 420
189 ggctctgagc agcacagcga cattgtgaag tttgtggtca aagactctc aaagctactc 480
190 aagaccaaga ctgaggcacc tacaacctg acataccct tgaaagcaac atctacagt 540
191 aagcagtcct gggactggac cactgacatg gatggctacc ttggagagac cagtgtctgg 600
192 ccaggaaaga gcctgcctgt ctttgccatc atcctcatca tctccttggt ctgtatggtg 660
193 gttttttacca tggcctatat catgctctgt cggaagacat cccaacaaga gcatgtctac 720
194 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaaccat gaggggtggc 780
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205 cagcttttaa ttgaaattgt tatttcacag gccagggttc agttctgtc ctccactata 1440
206 agtctaattg tctgactctc tcctggtgct caataaatat ctaatcataa cagcaaaaaa 1500
207 aaa 1503
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211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
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216 1 5 10 15
217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
218 20 25 30
219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
220 35 40 45

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221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
222      50                      55                      60
223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
224 65                      70                      75                      80
225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
226                      85                      90                      95
227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
228                      100                      105                      110
229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
230                      115                      120                      125
231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
232                      130                      135                      140
233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
234 145                      150                      155                      160
235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
236                      165                      170                      175
237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
238                      180                      185                      190
239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
240                      195                      200                      205
241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
242                      210                      215                      220
243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
244 225                      230                      235                      240
245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
246                      245                      250                      255
247 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
248                      260                      265                      270
249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
250                      275                      280                      285
251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
252                      290                      295                      300
253 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
254 305                      310                      315
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258 <211> LENGTH: 2181
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
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265 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
266 catcctggaa gtgccagaga gtgtaacagg accttggaag ggggatgtga atcttccttg 240
267 cacctatgac cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
268 ctacagacct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
269 gtaccagggc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaattgag 420
270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
271 tggcaaccaa gtcgtgagag ataagattac tgagctccgt gtccagaaac tctctgtctc 540
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